

1 ATGATTACAATAGTTTTTAAATCCTAGCCTATCTGCTGGGTTGCGATTCCATCTGGTCTCTGGATTGGACAAGTATTTCTTCAAATCAATCTACGGGAGC 100  
TACTAATGTTATCAAATAATTAGGATCGGATAGACGACCAAGCTAAGGTAGACGAGACCTAACCTGTTTCATAAGAAAGTTTAGTTAGTAGCGCTCG

1 M I T I V L L I L A Y L L G S I P S G L W I G Q V F F Q I N L R E H 34

101 ATGGTTCTGGTAACACTGGAAACGACCAACACCTTCGCAATTTAGGTAAGAAAGCTGGTATGGCAACCTTTGTGATTGACTTTTTCAAAGGAACCCCTAGC 200  
TACCAAGACCAATTGTGACCTTGTGCTGGTTGTGAAGGCGTAAATCCATTCTTCGACCATACCGTTGGAAACACTAACTGAATAAGTTTCCITGGGATCG

35 G S G N T G T T N T F R I L G K K A G M A T F V I D F F K G T L A 67

201 AACGCTGCTTCGGATTATTTTTCATCTAAGGGGTTTCTCCTCTCATCTTTGGACTTTTGGCTGTTATCGGCCATACCTTCCCTATCTTTGCGAGGATTT 300  
TTGGACGAAGGCTAATAAAGTAGATGTTCCGCAAGAGGAGTAGAAGCTGAAACCTGAAACCGACAATAGCCGATAGGAAGGATAGAAACGTCCTAAA

68 T L L P I I F H L Q G V S P L I F G L L A V I G H T F P I F A G F 100

301 AAAGGTGTAAGGCTGTGCAACAGTGTGGAGTGATTTTCGGATTTCGCTCTATCTTCTGTCTCTACCTTGGGATTATCTTCTTTGGAGCTCTCTATC 400  
TTTCCACCAATCCGACAGCGTTGGTCAGACCTCACTAAAGCCTAACCGGATAGAGACAGATGGAACGCTAATAGAAGAAACCTCGAGAGATAG

101 K G G K A V A T S A G V I F G F A P I F C L Y L A I I F F G A L Y L 134

401 TTGGCAGTATGATTTCACTGTCTAGTGTCAAGCATCGATTGGGGTGTATCGGGTCTGCTCTTCCACTTTTGGTTTTATCCTGAGTAACTATGA 500  
AACCGTCATACTAAGTGACAGATCACAGTGTGCTAGCTAACGCCGACAAATAGCCCCAAGACGAGAAAGGTGAAACCAACCAAAATAGGACTCATTGTGATACT

135 G S M I S L S S V T A S I A A V I G V L L F P L F G F I L S N Y D 167

501 CTCTCTTTCATCGCTATTATCTTAGCACTTGTAGTTGATTATCAATTCGTATAGGACAATATAGCTCGTATCAAAAATAAACTGAAAAATTTGGTC 600  
GAGAGAGAAGTAGGATAATAGATCGTGAACGATCAAACTAATAGTAAGCAGTATTCCTGTTATATCGAGCATAGTTTAAATTTTGAATTTTAAACCCAG

168 S L F I A I I L A L A S L I I I R H K D N I A R I K N K T E N L V 200

601 CCTTGGGGATTGAACTAACCCTCAAGATCCTAAAAATAA 642 SEQ ID NO:2  
GGAAACCCCTAACTTGGGATGTTCTAGGATTTTATT SEQ ID NO:11

201 P W G L N L T H Q D P K K • 213 SEQ ID NO:1

FIG. 1

1 ATGTTAATTGCTTTATTGATTATTTTGGCCTACTTGATAGGAGCATTCCATCTGGCTTAATTGTGGCAAGCTTGCCAAAGGAATTGATATTCGGGAGC 100  
TACAATTACGAAATAACTAATAAAACCGGATGAACCTATCCGTCGTAAAGGTAGACCGAATTAAACACCCGTTTGAACCGGTTTCTTAACTATAAGCCCTCG  
34  
1 M L I A L L I I L A Y L I I G S I P S G L I V G K L A K G I D I R E H 200  
ACGGAAGCGGCAACTTAGGCGCTACCAATGCAATTCGGTAAAGCTGGTTGGTCTGTCATAGCCGGAGATATTTTGAAGGAGACACTGGC  
TGCCTTCGCCGTTGAATCCGCGATGGTTACGTAAGGCATGTAAACCACTTTTCGACCAAGCCAGCAGTATCGGCCCTCTATAAACTTTTCCCTGTGACCG  
101  
35 G S G N L G A T N A F R T L G V K A G S V V I A G D I L K G T L A 300  
AACTGCATTGCCCTTTCTCATGTCATGTTGATATTACCCGCTTCTTGCCAGGAGTCTTTGGCGTTTATAGGCCACGTTTCCCATCTTCGCCAAATTTAA  
TTGACGTAAACGGAAGAAGTACGTACAACCTATAAGTGGGCGAAGACGTCCTCAGAAACGCCCAAAATCCGGTGCAAAAGGGTAGAAGCGGTTTAAATTT  
100  
68 T A L P F L M H V D I H P L L A G V F A V L G H V F P I F A K F K 400  
GGCGGTAAAGCCGTGGGACATCAGGAGCGTTTGTCTATTTACGCCACCCCTGTTATTTATCAGATGGTTGCGGTATTTCTTCATCTTTTATACTTGA  
CCGCCATTTCCGGCACCGCTGTAGTCTCCGCAAAACGATAAAATGCGTGGGACAAATAAATAGTGCTACCAACGCCCAATAAGAGTAGAATAATGAAC  
301  
101 G G K A V A T S G G V L L F Y A P L L F I T M V A V F F I F L Y L T 500  
CTAAATTTGTTTCTCTCATCGATGTTAAACAGGATCTATCTGTTATATATAGTTTCTTGTCCATGATACGTAATTTATTGATTGTTGTTACCCCTGCT  
401 GATTTAACNAAGAGAGTAGCTACAAATTTGTCCTAGATATGACAATATATATCAAAAGAACAGGTAATGCTATGCATAAATACTAACAGCAATGGGACGA  
167  
135 K F V S L S S M L T G I Y T V I Y S F F V H D T Y L L I V V T L L L SEQ ID NO:4  
501 CACTATTTTGTGATATACAGACACCGAGCGAACAATTAAACGAATTATCAATAAACAGAACCTAAAGTAAATGGTTATAA SEQ ID NO:12  
GTGATAAAACACTATATGCTGTGGCTCGCTTGTAAATTTGCTTAATAGTTATTTTGTCTTGGATTTTCAATTTTACCAATATT  
SEQ ID NO:3  
168 T I F V I Y R H R A N I K R I I N K T E P K V K W L . 193

FIG. 2

STRATEGY FOR TARGETED DELETIONS OF GENES  
IN *S. PNEUMONIAE*

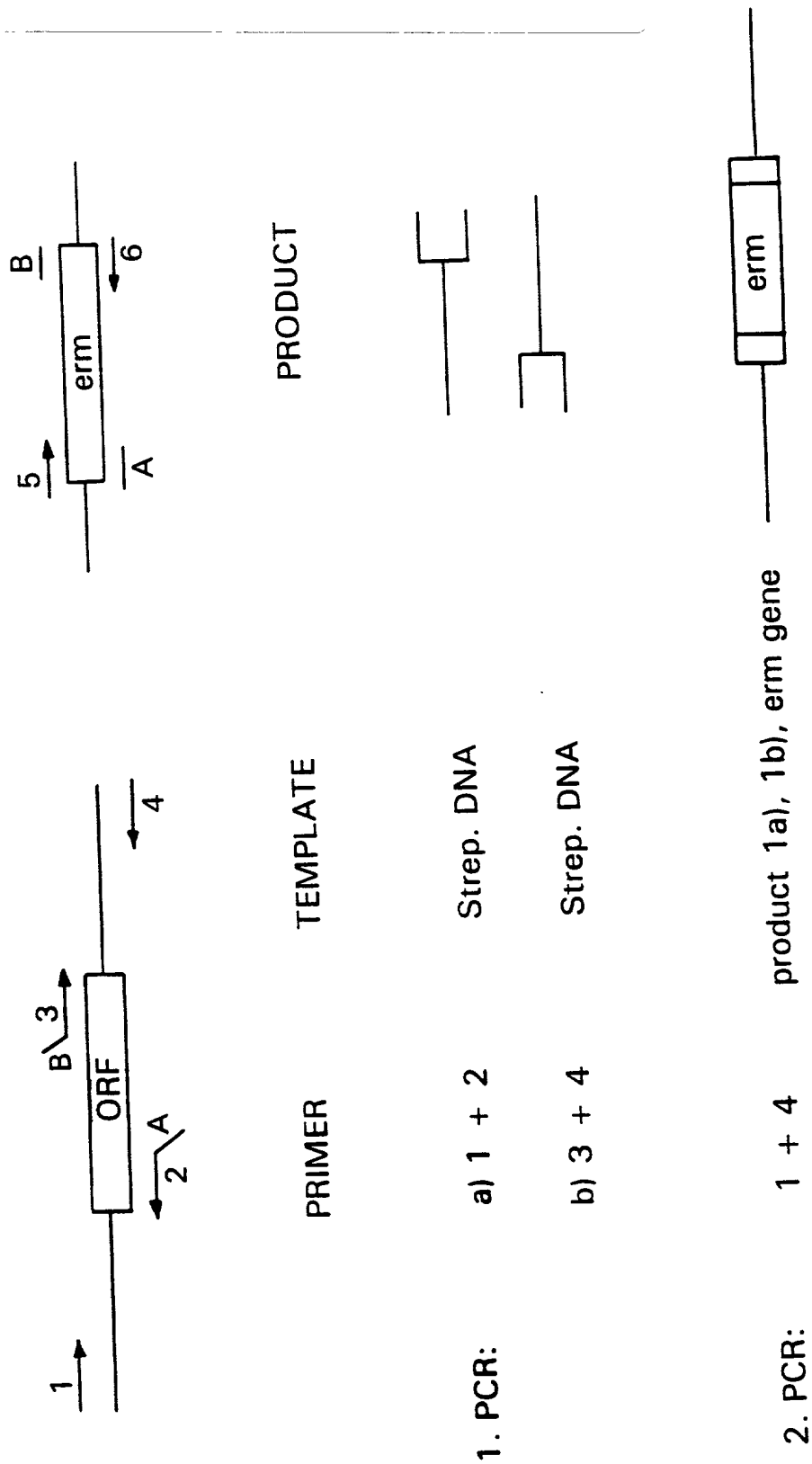
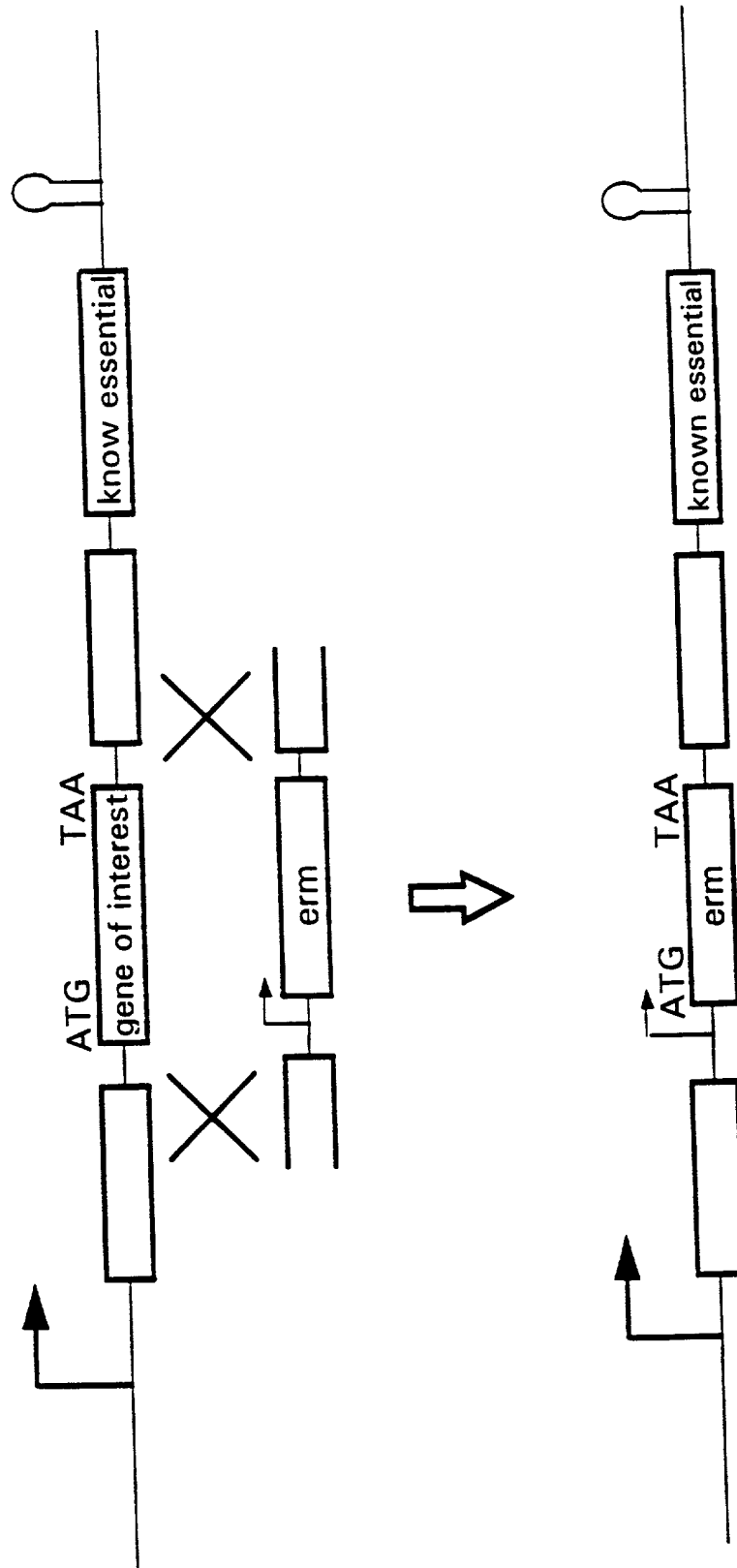


FIG. 3

## NON-POLAR GENE KNOCKOUTS IN *S. PNEUMONIAE*



**FIG. 4**